with acute tonsillopharyngitis (AT) and, unless adequately treated with antimicrobial therapy, it has been demonstrated that they can cause recurrent episodes of this disease. Moreover, it has recently been observed that the great majority of the children with a history of severely recurrent AT (and therefore considered eligible for elective tonsillectomy) are infected by atypical bacteria and that tonsillectomy seems to be effective in reducing the recurrence of both AT and acute respiratory disease in the presence of such infections. This means that treatment with macrolides can solve the acute illness and reduce the risk of new recurrences in the case of M. *pneumoniae* or *C. pneumoniae* infections and that appropriate treatment might postpone or abolish the need of tonsillectomy.

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36.002

Chlamydia trachomatis: Area Under the Iceberg

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In both sexes, genital *Chlamydia trachomatis* infection is still the most commonly reported bacterial sexually transmitted infectious disease worldwide. The prevalence is highest in persons aged less than 25 years. In females, up to 40% of chlamydial cervicitis might ascend to the endometrium, and is responsible for the etiology of endometritis and salpingitis. Late sequels of Fallopian tube involvement include pelvic inflammatory disease, ectopic pregnancy, tubal factor infertility and chronic pelvic pain. Since the overwhelming majority of primary infections (urethritis in men and cervicitis or urethritis in women) are asymptomatic, early diagnosis should essentially rely on annual screening of sexually active young women as well as men at high risk sexual behavior. At present, nucleic acid amplification techniques (NAAT) are the most sensitive tests for the detection of the pathogen in male and female biological samples. Over the last decade, administration of a single oral dose of 1000 mg azithromycin is the recommended treatment for uncomplicated primary genital chlamydial infection in men and women. In addition, azithromycin was shown to be as effective as amoxicillin or erythromycin for the eradication of C. trachomatis infection in pregnant women and this regimen resulted in less adverse events. In a recent multicenter study in Central and Eastern Europe, prevalence of endocervical chlamydial infection in women aged less than 25 years was 6%, with significant differences of frequencies among some geographical areas. Risk factors of infection were in accordance with those reported form other parts of Europe.

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Acne Vulgaris - Old/New Treatment?

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Acne vulgaris is one of the most frequent skin diseases affecting predominantly adolescents. The therapy depends on the severity of the disease. Systemic antibiotics in acne treatment have always been a controversial topic, as deprecated and respected at the same time. Pulse azithromycin therapy has devoted attention of many dermatologists. Several studies on this therapy were published so far, but dosage regimens in pulsed azithromycin therapy slightly differ between studies. However, all of them present that azithromycin has better clinical efficacy and safety than systemic minocycline or tetracycline. At our department, azithromycin has been administered and studied for four and half years now, with remarkable results. We have compared the effect of azithromycin against quinolones and tetracyclines. Three groups (30 patients each) of comparable age (aged 14—18 years) and gender suffering from moderate acne papulopostulosa (Cook's acne severity grading scale 2—6) were observed. Azithromycin was administered 500 mg orally during three subsequent days, followed by 500 mg weekly for the following six weeks. Ofloxacin was administered 100 mg for five days, 100 mg once daily following 10 days and 50 mg once daily during five weeks. Doxycycline was administered 100 mg twice daily for five days, 100 mg once daily for 10 days and 50 mg once daily following five weeks. Topical agents containing ichthamol and azelaic acid were applied. Significantly better results (reduction in inflammatory lesions) were observed after the third treatment week in the azithromycin group. The results remained significant even after therapy termination and at the follow-up visit (five months after therapy termination). Also, no adverse events were recorded in the azithromycin group.

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36.004

Acute Infectious Gastroenterocolitis: Use or Not to Use Antibiotics?

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Travelers' diarrhea (TD) is the leading cause of morbidity in travelers. This lecture will primarily address pediatric TD by discussing existing data on children as well as extrapolation of appropriate adult data and will propose reasonable therapeutic parameters for infants and children. TD is rarely associated with mortality though it is responsible for significant morbidity in traveling infants and children. Untreated, TD in children may last for days or even weeks. Prevention of TD generally includes dietary counseling and occasionally the use of chemoprophylaxis. The use of antimicrobial and antidiarrheal agents for the treatment of TD in children is controversial and there is still little data published and no firm recommendations available to guide the clin-

ician. Modern macrolide, azithromycin, is now commonly used as a sole agent for TD and is particularly effective against *Shigella spp.* and *Campylobacter spp.*, including *Campylobacter spp.* resistant to fluoroquinolones. A single-center, randomized, no treatment-controlled parallel group, assessor-blind trial was performed in children with *Campylobacter enterocolits* treated at the University Hospital for Infectious Diseases ''Dr Fran Mihaljevic'', Zagreb, Croatia. The primary objective was to evaluate the efficacy of a single oral azithromycin dose vs. standard oral erythromycin regimen or no antibiotic for *Campylobacter enterocolits* in children $\leq$12 years of age. The results of our study have shown that a single azithromycin 30 mg/kg administration early after disease onset effectively eradicates the pathogen and accelerates clinical cure in childhood *Campylobacter enterocolitis*. It is clinically superior to an early commenced 5-day erythromycin regimen.

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Biodiversity (invited)

37.001

Diversity of Human Microbial Pathogens and Commensals

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Complex microbial ecosystems occupy the cutaneous and mucosal surfaces of humans. Recent advances have highlighted both the tremendous diversity of these communities and their importance to host physiology, yet, we have only scratched the surface. Questions remain about the ecological processes that establish and maintain the human microbiota throughout life. Furthermore, basic features of the human microbial ecosystem remain poorly described, including variability in diversity, in space and time. Host individuality imposes a strong signature on patterns of diversity. In turn, our indigenous microbial ecosystem defines who we are as individuals. Assembly of the oral and the gut microbiota may also involve both stochastic historical events and contemporary environmental factors. Approaches that combine community ecology, molecular microbial ecology, and metagenomics may improve our understanding of health and disease within the communal human organism. By understanding the patterns of diversity associated with human health, we may be able to preserve and restore health more effectively. By recognizing the early signs of impending disturbance, we may be able to predict and avoid disease.

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37.002

Evolution of Diversity in Pathogen Populations

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Using sequencing or chip-based genomic approaches it is possible to gain insights into the genetic diversity and genome dynamics of bacterial pathogen populations. We study Bacillus anthracis, Yersinia pestis and Escherichia coli as model systems, all of which have several representative genome sequences available, allowing for the comparison of both clinical and environmental isolates. It allows to analyze the types of host variation, selection and adaptation occurring during the time course of a single or multiple outbreaks of human disease. Comparative analyses of the respective genome inventories and those of neighboring taxa and phyla, allows for the discovery of species- and lineage-specific microevolutionary traits and further elucidates common and unique traits in genome evolution and speciation. Applying SNP-based genotyping and resequencing methodologies, we were able to reconstitute a detailed evolutionary history of the B. anthracis, Y. pestis and the E. coli O157:H7 lineage and resolve highly clonal and monomorphic population structures. To study these subtle but important genetic variations, we have developed a bioinformatics pipeline that facilitates the discovery and validation of rare polymorphisms using genome sequence read coverage and quality. Analysis of the data led to an estimate of the degree of reductive evolution or the extent of influx of genetic material via horizontal gene transfer in these dynamic bacterial populations. In addition, it is possible to assess the impact of such alterations on the bacterial fitness, environmental survival and individual pathogenic potential. Although there is a stringent correlation between the absence of certain genes and a potential physiological function, the opposite does not hold true. Therefore, by studying the pan-genome of these important bacterial species, we can better define commensalism and pathogenicity as well as establish more accurate genetic species borders. Understanding genetic diversity and genome dynamics in bacterial pathogen populations has major impacts on the molecular epidemiology and microbial forensic communities and provides critical insights into the evolutionary and ecological niches of these human pathogens.

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37.003

Retroviral Biodiversity: Practical Consequences for HIV Treatment and Prevention

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Background: Retroviral diversity is attributable both to the infidelity of the reverse transcriptase (RT)enzyme that is responsible for transcribing the viral RNA genome into DNA as well as to a high viral replication rate. In the case of HIV-1, the error rate of RT is approximately 5×10^{-5}. Given a genomic length of 9.2 kb, this means that a mutation is likely to take place almost every time that HIV replicates; consequently, mutations are found throughout the HIV genome infected individuals. These mutations include those responsible for escape from immunological pressure as well as those associated with drug resistance. HIV replication patterns in different areas of the world have also given rise to a series of subtypes and recombinant forms that predominate in different geographic locales. Proper interpretation of drug resistance mutational patterns has potentiated both the sequencing of drugs within a given drug class, as well as